

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/713,928B

1646

DATE: 09/01/98  
TIME: 10:49:46

INPUT SET: S28333.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: RADIN, DAVID N.  
6 CRAMER, CAROLE L.  
7 OISHI, KAREN K.  
8 WEISSENBORN, DEBORAH L.  
9  
10 (ii) TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN  
11 PLANT-BASED EXPRESSION SYSTEMS  
12  
13 (iii) NUMBER OF SEQUENCES: 15  
14  
15 (iv) CORRESPONDENCE ADDRESS:  
16 (A) ADDRESSEE: Pennie & Edmonds  
17 (B) STREET: 1155 Avenue of the Americas  
18 (C) CITY: New York  
19 (D) STATE: New York  
20 (E) COUNTRY: USA  
21 (F) ZIP: 10036-2711  
22  
23 (v) COMPUTER READABLE FORM:  
24 (A) MEDIUM TYPE: Floppy disk  
25 (B) COMPUTER: IBM PC compatible  
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
28  
29 (vi) CURRENT APPLICATION DATA:  
30 (A) APPLICATION NUMBER: 08/713,928  
31 (B) FILING DATE: 13-SEP-1996  
32 (C) CLASSIFICATION:  
33  
34 (vii) PRIOR APPLICATION DATA:  
35 (A) APPLICATION NUMBER: US 60/003,737  
36 (B) FILING DATE: 14-SEP-1995  
37  
38 (viii) ATTORNEY/AGENT INFORMATION:  
39 (A) NAME: Coruzzi, Laura A.  
40 (B) REGISTRATION NUMBER: 30,742  
41 (C) REFERENCE/DOCKET NUMBER: 7956-0011-999  
42  
43 (ix) TELECOMMUNICATION INFORMATION:  
44 (A) TELEPHONE: (212) 790-9090  
45 (B) TELEFAX: (212) 869-9741  
46 (C) TELEX: 66141 PENNIE

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/713,928BDATE: 09/01/98  
TIME: 10:49:47

INPUT SET: S28333.raw

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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGTCTAGAG TAAGCATCAT GGCTGGC

27

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACGAATTCT GGCGACGCCA CAGGTAGGTG TGA

33

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/713,928B

DATE: 09/01/98  
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INPUT SET: S28333.raw

|     |  |      |
|-----|--|------|
| 100 | ATGGAGTTTT CAAGTCCTTC CAGAGAGGAA TGTCCCAAGC CTTTGAGTAG GGTAAGCATC  | 60   |
| 101 |  |      |
| 102 | ATGGCTGGCA GCCTCACAGG TTTGCTTCTA CTTCAGGCAG TGTCGTGGGC ATCAGGTGCC  | 120  |
| 103 |  |      |
| 104 | CGCCCCTGCA TCCCTAAAAG CTTCGGCTAC AGCTCGGTGG TGTGTGTCTG CAATGCCACA  | 180  |
| 105 |  |      |
| 106 | TACTGTGACT CCTTTGACCC CCCGACCTTT CCTGCCCTTG GTACCTTCAG CCGCTATGAG  | 240  |
| 107 |  |      |
| 108 | AGTACACGCA GTGGGCGACG GATGGGGCTG AGTATGGGGC CCATCCAGGC TAATCACACG  | 300  |
| 109 |  |      |
| 110 | GGCACAGGCC TGCTACTGAC CCTGCAGCCA GAACAGAAGT TCCAGAAAGT GAAGGGATTT  | 360  |
| 111 |  |      |
| 112 | GGAGGGGCCA TGACAGATGC TGCTGCTCTC AACATCCTTG CCCTGTCACC CCCTGCCCAA  | 420  |
| 113 |  |      |
| 114 | AATTTGCTAC TTAAATCGTA CTTCTCTGAA GAAGGAATCG GATATAACAT CATCCGGGTA  | 480  |
| 115 |  |      |
| 116 | CCCATGGCCA GCTGTGACTT CTCCATCCGC ACCTACACCT ATGCAGACAC CCCTGATGAT  | 540  |
| 117 |  |      |
| 118 | TTCCAGTTGC ACAACTTCAG CCTCCCAGAG GAAGATACCA AGCTCAAGAT ACCCCTGATT  | 600  |
| 119 |  |      |
| 120 | CACCGAGCCC TGCAGTTGGC CCAGCGTCCC GTTTCACTCC TTGCCAGCCC CTGGACATCA  | 660  |
| 121 |  |      |
| 122 | CCCCTTGGC TCAAGACCAA TGGAGCGGTG AATGGGAAGG GGTCACTCAA GGGACAGCCC   | 720  |
| 123 |  |      |
| 124 | GGAGACATCT ACCACCAGAC CTGGGCCAGA TACTTTGTGA AGTTCCTGGA TGCCTATGCT  | 780  |
| 125 |  |      |
| 126 | GAGCACAAGT TACAGTTCTG GGCAGTGACA GCTGAAAATG AGCCTTCTGC TGGGCTGTTG  | 840  |
| 127 |  |      |
| 128 | AGTGGATACC CCTTCCAGTG CCTGGGCTTC ACCCCTGAAC ATCAGCGAGA CTTTATTGCC  | 900  |
| 129 |  |      |
| 130 | CGTGACCTAG GTCCTACCCT CGCCAACAGT ACTCACCACA ATGTCCGCCT ACTCATGCTG  | 960  |
| 131 |  |      |
| 132 | GATGACCAAC GCTTGCTGCT GCCCCACTGG GCAAAGGTGG TACTGACAGA CCCAGAAGCA  | 1020 |
| 133 |  |      |
| 134 | GCTAAATATG TTCATGGCAT TGCTGTACAT TGGTACCTGG ACTTTCCTGGC TCCAGCCAAA | 1080 |
| 135 |  |      |
| 136 | GCCACCCTAG GGGAGACACA CCGCCTGTTC CCCAACACCA TGCTCTTTGC CTCAGAGGCC  | 1140 |
| 137 |  |      |
| 138 | TGTGTGGGCT CCAAGTTCTG GGAGCAGAGT GTGCGGCTAG GCTCCTGGGA TCGAGGGATG  | 1200 |
| 139 |  |      |
| 140 | CAGTACAGCC ACAGCATCAT CACGAACCTC CTGTACCATG TGGTCGGCTG GACCGACTGG  | 1260 |
| 141 |  |      |
| 142 | AACCTTGCCC TGAACCCCGA AGGAGGACCC AATTGGGTGC GTAACTTTGT CGACAGTCCC  | 1320 |
| 143 |  |      |
| 144 | ATCATTGTAG ACGTCACCAG GGACACGTTT TACAAACAGC CCATGTTCTA CCACCTTGGC  | 1380 |
| 145 |  |      |
| 146 | CACTTCAGCA AGTTCATTCC TGAGGGCTCC CAGAGAGTGG GGCTGGTTGC CAGTCAGAAG  | 1440 |
| 147 |  |      |
| 148 | AACGACCTGG ACGCAGTGGC ACTGATGCAT CCCGATGGCT CTGCTGTTGT GGTCGTGCTA  | 1500 |
| 149 |  |      |
| 150 | AACCGCTCCT CTAAGGATGT GCCTCTTACC ATCAAGGATC CTGCTGTGGG CTTCTTGGAG  | 1560 |
| 151 |  |      |
| 152 | ACAATCTCAC CTGGCTACTC CATTACACC TACCTGTGGC GTCGCCAGAA TTCGGACTAC   | 1620 |

# RAW SEQUENCE LISTING

## PATENT APPLICATION US/08/713,928B

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153
154 AAGGACGACG ATGACAAGTT GA 1642
155
156 (2) INFORMATION FOR SEQ ID NO:4:
157
158 (i) SEQUENCE CHARACTERISTICS:
159 (A) LENGTH: 546 amino acids
160 (B) TYPE: amino acid
161 (C) STRANDEDNESS: single
162 (D) TOPOLOGY: unknown
163
164 (ii) MOLECULE TYPE: peptide
165
166
167
168
169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
170
171 Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser
172 1 5 10 15
173
174 Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
175 20 25 30
176
177 Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
178 35 40 45
179
180 Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
181 50 55 60
182
183 Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
184 65 70 75 80
185
186 Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
187 85 90 95
188
189 Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
190 100 105 110
191
192 Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
193 115 120 125
194
195 Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
196 130 135 140
197
198 Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
199 145 150 155 160
200
201 Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
202 165 170 175
203
204 Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
205 180 185 190

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# RAW SEQUENCE LISTING PATENT APPLICATION US/08/713,928B

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|-----|---|
| 206 |   |
| 207 | Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln |
| 208 | 195 200 205   |
| 209 |   |
| 210 | Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu |
| 211 | 210 215 220   |
| 212 |   |
| 213 | Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro |
| 214 | 225 230 235 240   |
| 215 |   |
| 216 | Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu |
| 217 | 245 250 255   |
| 218 |   |
| 219 | Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu |
| 220 | 260 265 270   |
| 221 |   |
| 222 | Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu |
| 223 | 275 280 285   |
| 224 |   |
| 225 | Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly |
| 226 | 290 295 300   |
| 227 |   |
| 228 | Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu |
| 229 | 305 310 315 320   |
| 230 |   |
| 231 | Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr |
| 232 | 325 330 335   |
| 233 |   |
| 234 | Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr |
| 235 | 340 345 350   |
| 236 |   |
| 237 | Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg |
| 238 | 355 360 365   |
| 239 |   |
| 240 | Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser |
| 241 | 370 375 380   |
| 242 |   |
| 243 | Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met |
| 244 | 385 390 395 400   |
| 245 |   |
| 246 | Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly |
| 247 | 405 410 415   |
| 248 |   |
| 249 | Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp |
| 250 | 420 425 430   |
| 251 |   |
| 252 | Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Val Thr Lys Asp |
| 253 | 435 440 445   |
| 254 |   |
| 255 | Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys |
| 256 | 450 455 460   |
| 257 |   |
| 258 | Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys |

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/713,928B**

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Original Text